ION CHANNELS

Technical field

The present invention relates to proton or acid-sensing ion channels and nucleic acid encoding the same. It further relates to methods and materials for generating and using these.

Prior art

Acidosis accompanies many painful inflammatory and ischaemic conditions. The pain caused by acids is thought to be mediated in part by H+-gated cation channels present in sensory neurons. Thus H+-gated cation channels are of interest, *inter alia*, in the treatment of inflammation or other painful conditions e.g. through the use of targeted analgesics.

One H+-gated channel (ASIC, for acid-sensing ionic channel) has been cloned from rat (Waldmann *et al.* (1997) Nature 386, 6621, p173-177. This belongs to the amiloride-sensitive Na+ channel/degenerin family of ion channels (see Waldmann and Lazdunski 1998, Current Biology 8: 418-424).

Heterologous expression of ASIC induces an amiloride-sensitive cation (Na+ > Ca2+> K+) channel which is transiently activated by rapid extracellular acidification. The biophysical and pharmacological properties of the ASIC channel closely match one of the H+-gated cation channels described in sensory neurons. However ASIC is also distributed widely throughout the brain.

Owing to the interest in H+-gated cation channels, it will be appreciated that the provision of a new channel, particularly one having one or more novel activities compared to those already available to the public, would provide a contribution to the art.

Disclosure of the invention

The present inventors have now cloned nucleic acid encoding a novel H+-gated cation channel from a rat sensory neuron cDNA library, and isolated and characterised the encoded protein. The nucleic acid sequence is shown as Seq ID No 1, while the encoded protein is Seq ID No 2. The channel, which is present in both spinal cord and throughout the central nervous system in subsets of neurons, is hereinafter referred to as "SPASIC".

Briefly the inventors used molecular cloning techniques to characterise the SPASIC protein. *In situ* DNA hybridisation and RNA Northern blotting showed that the new channel transcripts are present in dorsal root ganglion neurons and in central nervous system tissues. When expressed in transfected COS cells, the channel mediated both a transient and a sustained flow of current when exposed to extracellular acidity, e.g. of below pH 7.0.

SPASIC shares 43% sequence identity with ASIC (the amino acid sequence of which is shown as Seq ID No 3) and has similarities with other characterised ASIC-type proteins (see Figure 1). However SPASIC has unique properties. In particular it exhibits both a rapid, and then a sustained cation current in response to low pH. No H+-gated channel having these properties has been characterised

before.

Because of the expression of SPASIC in sensory neurons and the importance of proton-gated channels in pain and inflammation, this new channel is an analgesic drug target and has utility, *inter alia*, in screening techniques for identifying novel analgesic and anti-inflammatory agents.

Interestingly, its presence in subsets of central nervous system neurons also suggests an important role as a receptor or an autoreceptor involved in the regulation of neurotransmitter release or neuronal excitability or excitotoxicity. For instance, it is known that low pH is also found in synaptic vesicles, and the release of neurotransmitters is associated with the release of protons. Proton gated cation channels have been reported in isolated cells of the hypothalamus. Low pH has been found to be neuroprotective in some seizure models (Valiseck et al. Brain Research 1995 Feb 13; 671(2):245-253) and to regulate synaptic efficacy (Velisek et al. Hippocampus 1998; 8(1):24-32). Thus the channel also has utility in screening for agents that regulate neurotransmitter release or neuronal excitability, including the regulation of excitotoxicity and synaptic efficacy (e.g. in the context of learning and memory, cognition, perception, pain etc, depending *inter alia* on the location in which the channel may be expressed).

These and other aspects of the present invention will now be discussed in more detail.

Thus in a first aspect of the present invention there is provided an acid sensitive cation channel protein which is capable of reversibly mediating (i) a rapid, and (ii)

a sustained cation current.

Proteins, or polypeptides, of the present invention may be provided in recombinantly produced, isolated, enriched or cell-free form. They may be present in cells heterologously, which is to say that they do not naturally occur there, but have been introduced through human intervention.

By "acid sensitive" is meant that the cation permeability of the channel can be significantly increased by lowering the pH (increasing acidity, or reducing alkalinity).

The mediated current will occur in two phases, a "rapid" phase, and a "sustained" phase. Generally the rapid phase will last less than 500 milliseconds, more commonly less than about 200 milliseconds. The sustained phase will generally continue for the period in which the pH stimulus is maintained.

The two phase activity can be assessed by those skilled in the art without undue burden, for instance using voltage clamping techniques analogous to those described herein to analyse membranes or membrane preparations (e.g. from eucaryotic cells) into which the protein has been expressed or otherwise introduced. Some generally applicable methods are discussed in "Ionic Channels of Excitable Membranes" Hille, B. - Pub 1992, Sinauer.

Preferably the protein will have the electrophysiological and pharmacological characteristics of the SPASIC protein described herein. Preferably the protein comprises amino acid sequence Seq ID No 2.

In a further aspect of the invention there is disclosed a

SPASIC variant protein having ion channel activity and comprising an amino acid sequence having at least about 50%, or 60%, or 70%, or 80% homology, most preferably at least about 90%, 95%, 96%, 97%, 98% or 99% sequence identity with Seq ID No 2.

Ion channel activity may be tested as described above, using appropriate stimuli if required.

Similarity (or identity, or homology) may be as defined and determined by the TBLASTN program, of Altschul *et al.* (1990) *J. Mol. Biol.* 215: 403-10, which is in standard use in the art, or, and this may be preferred, the standard program BestFit, which is part of the Wisconsin Package, Version 8, September 1994, (Genetics Computer Group, 575 Science Drive, Madison, Wisconsin, USA, Wisconsin 53711). BestFit makes an optimal alignment of the best segment of similarity between two sequences. Optimal alignments are found by inserting gaps to maximize the number of matches using the local homology algorithm of Smith and Waterman.

Homology may be over the full-length of the relevant sequence shown herein, or may be over a part of it, preferably over a contiguous sequence of about or greater than about 20, 25, 30, 33, 40, 50, 67, 133, 167, 200, 233 or more amino acids or compared with Seq ID No 2.

Thus a variant polypeptide in accordance with the present invention may include within the sequence shown in Seq ID No 2, a single amino acid or 2, 3, 4, 5, 6, 7, 8, or 9 changes, about 10, 15, 20, 30, 40 or 50 changes, or greater than about 50, 60, 70, 80 or 90 changes. In addition to one or more changes within the amino acid sequence shown, a variant polypeptide may include

additional amino acids at the C-terminus and/or N-terminus. Alternatively it may represent an active (as an ion channel) fragment of the protein e.g. a pore forming fragment.

Proteins or polypeptides of the present invention may be prepared by the expression of nucleic acids encoding therefor in appropriate host cells, as described in more detail hereinafter..

Thus in a further aspect of the present invention there is provided nucleic encoding a protein of the invention as described above.

Nucleic acid according to the present invention may include cDNA, RNA, genomic DNA and modified nucleic acids or nucleic acid analogs (e.g. peptide nucleic acid). Where a DNA sequence is specified, e.g. with reference to a figure, unless context requires otherwise the RNA equivalent, with U substituted for T where it occurs, is encompassed.

Nucleic acid molecules according to the present invention may be provided isolated and/or purified from their natural environment, in substantially pure or homogeneous form, or free or substantially free of other nucleic acids of the species of origin. Where used herein, the term "isolated" encompasses all of these possibilities.

The nucleic acid molecules may be wholly or partially synthetic. In particular they may be recombinant in that nucleic acid sequences which are not found together in nature (do not run contiguously) have been ligated or otherwise combined artificially. Alternatively they may have been synthesised directly e.g. using an automated

synthesiser.

Thus in one embodiment of this aspect of the invention there is provided a nucleic acid encoding SPASIC e.g. a nucleic acid encoding Seq ID No 2 (which nucleic acid sequence is set out as bases 292-1909 in Seq ID No 1). In another embodiment there is disclosed a sequence degeneratively equivalent to that sequence.

In another embodiment there is disclosed a nucleic acid which encodes a SPASIC variant as described above. Generally this will share homology or identity with the SPASIC encoding sequence in similar terms as are described in relation to the variant proteins above, but wherein amino changes correspond to changes in codons or individual nucleotides.

Variants may include distinctive parts or fragment (however produced) corresponding to a portion of the sequence provided. The fragments may encode particular functional parts of the polypeptide.

Equally the fragments may have utility in probing for, or amplifying, the sequence provided or closely related ones. Suitable lengths of fragment, and conditions, for such processes are discussed in more detail below.

Also included are nucleic acids which have been extended at the 3' or 5' terminus with respect any of these embodiments.

Preferred variant nucleic acids are those which, in addition to encoding SPASIC variants, are capable of hybridizing with at least one poly- or oligonucleotide of sequence selected from sequence of SEQ ID No 1 under low

stringency conditions, more preferably being capable of hybridizing with one or more of such sequences under high stringency conditions.

The expressions 'low stringency conditions' and 'high stringency conditions' will be understood by those skilled in the art, but are conveniently exemplified as set out in US 5202257, Col 9-Col 10. For instance, screening may initially be carried out under conditions, which comprise a temperature of about 37°C or less, a formamide concentration of less than about 50%, and a moderate to low salt (e.g. Standard Saline Citrate ('SSC') = 0.15 M sodium chloride; 0.15 M sodium citrate; pH 7) concentration.

Alternatively, a temperature of about 50°C or less and a high salt (e.g. 'SSPE'= 0.180 mM sodium chloride; 9 mM disodium hydrogen phosphate; 9 mM sodium dihydrogen phosphate; 1 mM sodium EDTA; pH 7.4). Preferably the screening is carried out at about 37°C, a formamide concentration of about 20%, and a salt concentration of about 5 X SSC, or a temperature of about 50°C and a salt concentration of about 2 X SSPE. These conditions will allow the identification of sequences which have a substantial degree of homology (similarity, identity) with the probe sequence, without requiring the perfect homology for the identification of a stable hybrid.

Suitable conditions include, e.g. for detection of sequences that are about 80-90% identical, hybridization overnight at 42°C in 0.25M Na_2HPO_4, pH 7.2, 6.5% SDS, 10% dextran sulfate and a final wash at 55°C in 0.1X SSC, 0.1% SDS. For detection of sequences that are greater than about 90% identical, suitable conditions include hybridization overnight at 65°C in 0.25M Na_2HPO_4, pH 7.2,

6.5% SDS, 10% dextran sulfate and a final wash at 60°C in 0.1X SSC, 0.1% SDS.

Sequence variants which occur naturally may include alleles (which will include polymorphisms or mutations at one or more bases) or pseudoalleles. Also included within the scope of the present invention would be isogenes, or other homologous genes sharing the requisite identity with SPASIC. The term 'variant' nucleic acid as used herein encompasses all of these possibilities.

In a further aspect of the present invention there is provided a method of identifying and/or cloning a nucleic acid according to the present invention which method employs Seq ID No 1 or a distinctive fragment thereof.

In one embodiment, nucleotide sequence information provided herein may be used in a data-base (e.g. of expressed sequence tags, or sequence tagged sites) search to find homologous sequences, such as those which may become available in due course, and expression products of which can be tested for activity as described below.

In a further embodiment, a variant in accordance with the present invention is also obtainable by means of a method which includes:

(a) providing a preparation of nucleic acid, e.g. from spinal cord,

(b) providing a nucleic acid molecule having a nucleotide sequence shown in or complementary to Seq ID No 1 or a distinctive fragment thereof,

(c) contacting nucleic acid in said preparation with said nucleic acid molecule under conditions for hybridisation of said nucleic acid molecule to any said gene or homologue in said preparation, and identifying said gene

or homologue if present by its hybridisation with said nucleic acid molecule.

Probing may optionally be done by means of so-called 'nucleic acid chips' (see Marshall & Hodgson (1998) Nature Biotechnology 16: 27-31, for a review).

Nucleic acids of the invention may be amplified from template DNA from cells using a specific DNA amplification reaction with specific primers targeted to amplify the DNA required, e.g. of SEQ ID No 1, e.g. from genomic DNA, spinal cord or DRG cDNA, or mRNA templates, e.g. by using polymerase chain reaction or, from RNA, by using reverse transcription (RT) followed by polymerase chain reaction (PCR)(see "PCR protocols; A Guide to Methods and Applications", Eds. Innis et al, Academic Press, New York, 1990).

Thus a method involving use of PCR in obtaining nucleic acid according to the present invention may include:
(a) providing a preparation of nucleic acid, e.g. from the CNS, or other appropriate tissue or organ,
(b) providing a pair of nucleic acid molecule primers useful in (i.e. suitable for) PCR, at least one of said primers having a sequence shown in or complementary to a sequence shown in Seq ID No 1 or a distinctive fragment thereof,
(c) contacting nucleic acid in said preparation with said primers under conditions for performance of PCR,
(d) performing PCR and determining the presence or absence of an amplified PCR product. The presence of an amplified PCR product may indicate identification of a variant.

Where it is desired to screen tissue derived libraries of

genomic DNA or cDNA or mRNA for DNA or RNA of the invention it will be convenient to use low then high stringency hybridization techniques as indicated above. Such screening may be carried out using hybridization probes targeted at all or part of SEQ ID No 1. Alternatively specific amplification primers (ie. PCR primers) as described above may be used to amplify homologous sequences native to the source DNA to be used as PCR template and the product DNA may be used as a specific probe when labelled to identify DNA of the invention from the genomic, cDNA or mRNA library material.

In each case, if need be, clones or fragments identified in the search can be extended. For instance if it is suspected that they are incomplete, the original DNA source (e.g. a clone library, mRNA preparation etc.) can be revisited to isolate missing portions e.g. using sequences, probes or primers based on that portion which has already been obtained to identify other clones containing overlapping sequence.

Distinctive fragments or oligonucleotides for use in probing or PCR may be selected prepared by those skilled in the art without burden in the light of the present disclosure. Typically they may be about 10 to 30 or fewer nucleotides in length (e.g. 18, 21 or 24). Generally specific primers are upwards of 14 nucleotides in length. For optimum specificity and cost effectiveness, primers of 16-24 nucleotides in length may be preferred. If required, probing can be done with entire restriction fragments of the gene diclosed herein which may be 100's or even 1000's of nucleotides in length.

For the purpose of identifying DNA coding for other ASIC-related proteins, it may be preferred to use probes and primers capable of hybridizing with those regions of the SEQ ID No 1 which are highly conserved between SPASIC and other ion channels (DRASIC, α-ASIC, β-ASIC). These regions can be identified from the amino acid sequence alignments disclosed herein. Highly conserved, as will be understood by those skilled in the art, means that degenerate primers can be devised which will amplify nucleic acids having the sequence characteristics of both SPASIC and the other ion channel.

For the purpose of identifying DNA encoding proteins having the currently-unique properties of SPASIC, it may be convenient to use probes or primers corresponding to all or a major part of the sequence of SEQ ID No 1, or to those parts of the sequence that are not well conserved between the different types of ASIC channel protein. Example regions include those amplified by the primers set out herein.

Preferred Examples are shown in Seq ID Nos 4 to 9. These are adapted to amplify the entire ORF (Seq ID No 4 and 5), a unique SPASIC portion for probing (Seq ID No 6 and 7) and degenerate primers having utility in finding new members of the ASIC family (Seq ID No 8 to 9).

Further suitable sequences for probes and primers of the invention will occur to those skilled in the art by alignment of the present sequence SEQ ID No 1 with the other known ASIC protein sequences. It will be realised that, where the nucleic acids of the present invention are provided in double stranded form, such probes and primers may be targeted at either strand.

Such probes, primers and oligonucleotides are provided by a further aspect of the invention and may be used in amplification reactions, or Southern or Northern blotting procedures.

Artificial variants (derivatives) may be prepared by those skilled in the art on the basis of the sequences provided herein, for instance by site directed or random mutagenesis, or by direct synthesis. Preferably the variant nucleic acid is generated either directly or indirectly (e.g. via one or amplification or replication steps) from an original nucleic acid having all or part of the sequence shown in Seq ID No 1.

Thus in a further aspect of the invention there is disclosed a method of producing a derivative nucleic acid comprising the step of modifying the coding sequence of Seq ID No 1.

Changes to a sequence, to produce a derivative, may be by one or more of addition, insertion, deletion or substitution of one or more nucleotides in the nucleic acid, leading to the addition, insertion, deletion or substitution of one or more amino acids in the encoded polypeptide.

Changes may be desirable for a number of reasons, including introducing or removing the following features: restriction endonuclease sequences; codon usage; other sites which are required for post translation modification; cleavage sites in the encoded polypeptide; motifs in the encoded polypeptide for post-translational modification. Leader or other targeting sequences (e.g. membrane or golgi locating sequences) may be added to the expressed protein to determine its location following

expression. All of these may assist in efficiently cloning and expressing an active polypeptide in recombinant form (as described below).

Other desirable mutation may be random (e.g. chemical) or site directed mutagenesis in order to alter the activity (e.g. specificity) or stability of the encoded polypeptide. For such methods, for example, a vectorised DNA of SEQ ID No 1 is exposed to a mutagenic material such as hydroxylamine, or, in the case of SDM, a PCR reaction is carried out on that DNA using a mutagenic primer, whereby DNA is produced which encodes for a protein different in sequence to SEQ ID No 2 at a few predictable or predetermined sites respectively.

Particular target areas of the sequence are those which may determine any of the following: specificity of activation of the ion channel (e.g. required pH change); nature of response (e.g. transient, sustained current); specificity of ion channel (e.g. relative permeability to different cations).

All of these properties can be tested, without burden, e.g. using appropriate voltage clamping techniques.

Preferably the amino acid sequence differs from SEQ ID No 2 only by conservative substitutions. The expression 'conservative substitutions' as used with respect to amino acids relates to the substitution of a given amino acid by an amino acid having physicochemical characteristics in the same class. Thus where an amino acid in SEQ ID No 2 has a hydrophobic characterising group, a conservative substitution replaces it by another amino acid also having a hydrophobic characterising group; other such classes are those where the

characterising group is hydrophilic, cationic, anionic or contains a thiol or thioether. Such substitutions are well known to those of ordinary skill in the art, i.e. see US 5380712, and are only contemplated where the resultant protein has ion channel activity.

Also included are variants having non-conservative substitutions. As is well known to those skilled in the art, substitutions to regions of a peptide which are not critical in determining its conformation may not greatly affect its activity because they do not greatly alter the peptide's three dimensional structure. In regions which are critical in determining the peptides conformation or activity such changes may confer advantageous properties on the polypeptide.

A quite different approach may include mixing or incorporating sequences from related ASIC-type genes into the SPASIC sequence. For example restriction enzyme fragments of SPASIC could be ligated together with fragments of a SPASIC homologue or even of an unrelated gene to generate recombinant variants of SPASIC (so called 'DNA shuffling' - see Crameri et al., 1998, Nature *391*.).

In one aspect of the present invention, the nucleic acids of the present invention are in the form of a recombinant and preferably replicable constructs, such as vectors.

"Vector" is defined to include, inter alia, any plasmid, cosmid, phage or other vector in double or single stranded linear or circular form which may or may not be self transmissible or mobilizable, and which can transform prokaryotic or eukaryotic host either by integration into the cellular genome or exist

extrachromosomally (e.g. autonomous replicating plasmid with an origin of replication).

Specifically included are shuttle vectors by which is meant a DNA vehicle capable, naturally or by design, of replication in two different host organisms, which may be selected from actinomycetes and related species, bacteria and eucaryotic (e.g. mammalian, yeast or fungal cells).

A vector including nucleic acid according to the present invention need not include a promoter or other regulatory sequence, particularly if the vector is to be used to introduce the nucleic acid into cells for recombination into the genome.

Preferably the nucleic acid in the vector is under the control of, and operably linked to, an appropriate promoter or other regulatory elements for transcription in a host cell such as a microbial, e.g. bacterial cell. The vector may be a bi-functional expression vector which functions in multiple hosts. In the case of genomic SPASIC DNA (isolatable as described above) this may contain its own promoter or other regulatory elements and in the case of cDNA this may be under the control of an appropriate promoter or other regulatory elements for expression in the host cell.

By "promoter" is meant a sequence of nucleotides from which transcription may be initiated of DNA operably linked downstream (i.e. in the 3' direction on the sense strand of double-stranded DNA).

"Operably linked" means joined as part of the same nucleic acid molecule, suitably positioned and oriented for transcription to be initiated from the promoter.

DNA operably linked to a promoter is "under transcriptional initiation regulation" of the promoter.

Thus this aspect of the invention provides a gene construct, preferably a replicable vector, comprising a promoter operatively linked to a nucleotide sequence provided by the present invention, such as the SPASIC gene (see Seq ID NO 1) or a variant thereof.

Generally speaking, those skilled in the art are well able to construct vectors and design protocols for recombinant gene expression. Suitable vectors can be chosen or constructed, containing appropriate regulatory sequences, including promoter sequences, terminator fragments, polyadenylation sequences, enhancer sequences, marker genes and other sequences as appropriate. For further details see, for example, *Molecular Cloning: a Laboratory Manual:* 2nd edition, Sambrook *et al*, 1989, Cold Spring Harbor Laboratory Press.

Many known techniques and protocols for manipulation of nucleic acid, for example in preparation of nucleic acid constructs, mutagenesis (see above discussion in respect of variants), sequencing, introduction of DNA into cells and gene expression, and analysis of proteins, are described in detail in *Current Protocols in Molecular Biology*, Second Edition, Ausubel et al. eds., John Wiley & Sons, 1992. The disclosures of Sambrook et al. and Ausubel et al. are incorporated herein by reference.

In one embodiment of this aspect of the present invention provides a gene construct, preferably a replicable vector, comprising an inducible promoter operatively linked to a nucleotide sequence provided by the present invention, such as Seq ID No 1.

The term "inducible" as applied to a promoter is well understood by those skilled in the art. In essence, expression under the control of an inducible promoter is "switched on" or increased in response to an applied stimulus. The nature of the stimulus varies between promoters. Some inducible promoters cause little or undetectable levels of expression (or no expression) in the absence of the appropriate stimulus. Other inducible promoters cause detectable constitutive expression in the absence of the stimulus. Whatever the level of expression is in the absence of the stimulus, expression from any inducible promoter is increased in the presence of the correct stimulus.

Particularly preferred are vectors suitable for expression of mammalian DNA, such as will occur to those skilled in the art, e.g. HSV or vaccinia vectors, or pcDNA3 shuttle vectors, e.g. as included within the lambda express system (Stratagene), which are capable of expressing heterologous protein in both bacteria and in eucaryotic cells such as COS cells. Suitable bacterial vectors will include lambda-Zap vectors such as the lambda-Zap-II vector available from Stratagene Cloning Systems. Bacterial clones containing plasmids capable of gene expression can be obtained by excising pBluescript from the lambda-Zap-II construct in the presence of a filamentous helper phage also available from Stratagene. Typical protocols are provided in the examples below, or in commercially available Stratagene kits.

A further aspect of the present invention provides cells containing, or more preferably transformed with (or transfected with) the nucleic acids of the present invention. Such cells are provided by transformation of a host cell, preferably a eucaryotic cell, e.g. a COS, CHO

or HEK 293 cell or an oocyte, preferably a Xenopus oocyte, particularly COS cells, using DNA of the invention as incorporated by recombinant DNA techniques into a vector or as directly incorporated into the cells' genomic DNA e.g. by electroporation or other such DNA integrating technique.

Such cells may be capable of expressing, or having expressed, a SPASIC protein as described hereinabove. The cells may thus mimic, in some respects, the electrophysiological and pharmacological properties of native SPASIC-expressing cells

It is also possible to produce cells bearing the receptor protein of the invention by direct injection of RNA of the present invention, into the cells wherein it becomes translated. In the case of Xenopus oocytes it is possible to achieve the presence of functioning SPASIC protein on cell membranes within 3 days such that it is ready for electrophysiological and pharmacological study.

The foregoing discussion has been generally concerned with uses of the nucleic acids of the present invention for production of functional polypeptides, thereby increasing the SPASIC or related ion channel activity in the cell.

However the information disclosed herein may also be used to reduce the activity of SPASIC or variants thereof in cells in which it is desired to do so.

For instance down-regulation of expression of a target gene may be achieved using anti-sense technology.

In using anti-sense genes or partial gene sequences to

down-regulate gene expression, a nucleotide sequence is placed under the control of a promoter in a "reverse orientation" such that transcription yields RNA which is complementary to normal mRNA transcribed from the "sense" strand of the target gene. See, for example, Rothstein et al, 1987; Smith *et al*, (1988) *Nature* 334, 724-726; Zhang *et al*, (1992) *The Plant Cell* 4, 1575-1588, English *et al*., (1996) *The Plant Cell* 8, 179-188. Antisense technology is also reviewed in Bourque, (1995), *Plant Science* 105, 125-149, and Flavell, (1994) *PNAS USA* 91, 3490-3496.

"Complementary to" means that the capable of base pairing with whereby A is the complement of T (and U); G is the complement of C.

An alternative to anti-sense is to use a copy of all or part of the target gene inserted in sense, that is the same, orientation as the target gene, to achieve reduction in expression of the target gene by co-suppression.

Further options for down regulation of gene expression include the use of ribozymes, e.g. hammerhead ribozymes, which can catalyse the site-specific cleavage of RNA, such as mRNA (see e.g. Jaeger (1997) "The new world of ribozymes" Curr Opin Struct Biol 7:324-335, or Gibson & Shillitoe (1997) "Ribozymes: their functions and strategies form their use" Mol Biotechnol 7: 242-251.)

Methods for producing regulatory sequences will involve no burden to those skilled in the art in the light of the present disclosure. Anti-sense or sense or ribozyme based regulation may be performed using vectors as described above, and may itself be regulated by employing

an inducible promoter in an appropriate construct. For instance incorporation of this DNA into mammalian cells might be readily accomplished using vectors, e.g. such as HSV, vaccinia or adenovirus (see Principles of Gene Manipulation (1994) 5th Edit. Old and Primrose 5th Edition, Blackwell Scientific Publications).

The complete sequence corresponding to the coding sequence (in reverse orientation for anti-sense) need not be used. For example fragments of sufficient length may be used. It is a routine matter for the person skilled in the art to screen fragments of various sizes and from various parts of the coding sequence to optimise the level of anti-sense inhibition. It may be advantageous to include the initiating methionine ATG codon, and perhaps one or more nucleotides upstream of the initiating codon. A further possibility is to target a conserved sequence of a gene, e.g. a sequence that is characteristic of one or more genes, such as a regulatory sequence.

The sequence employed may be about 500 nucleotides or less, possibly about 400 nucleotides, about 300 nucleotides, about 200 nucleotides, or about 100 nucleotides. It may be possible to use oligonucleotides of much shorter lengths, 14-23 nucleotides, although longer fragments, and generally even longer than about 500 nucleotides are preferable where possible, such as longer than about 600 nucleotides, than about 700 nucleotides, than about 800 nucleotides, than about 1000 nucleotides or more.

It may be preferable that there is complete sequence identity in the sequence used for down-regulation of expression of a target sequence, and the target sequence,

although total complementarity or similarity of sequence is not essential. One or more nucleotides may differ in the sequence used from the target gene. Thus, a sequence employed in a down-regulation of gene expression in accordance with the present invention may be a wild-type sequence (e.g. gene) selected from those available, or a variant of such a sequence.

The sequence need not include an open reading frame or specify an RNA that would be translatable. It may be preferred for there to be sufficient homology for the respective anti-sense and sense RNA molecules to hybridise. There may be down regulation of gene expression even where there is about 5%, 10%, 15% or 20% or more mismatch between the sequence used and the target gene. Effectively, the homology should be sufficient for the down-regulation of gene expression to take place.

One embodiment of this aspect of the invention employs DNA oligonucleotides, typically being of 10 to-30-bases long, conveniently about 20 bases long, optionally in degradation protected form, e.g. by being thiolated, and which conveniently have been chemically synthesized to be directed to hybridize with a part of the 5' coding region of the SPASIC mRNA. Annealing with the oligomeric DNA causes the mRNA to be degraded by activation of RNase H, or blocks the translation of the mRNA into protein. The small size of such oligomers facilitates their direct access into target cells which express the present ASIC proteins.

An alternative embodiment produces antisense RNA in vivo by inserting a tissue specific inducible or constitutively active promoter, enhancer or locus control region or element upstream of the coding region, or part

of the coding region, of DNA of SEQ ID No 1 in a construct which is then cloned into a vector. For use in mammals in therapy such a vector should be capable of infecting but not killing target cells. Convenient vectors for use in this embodiment, which can target mammalian dorsal root ganglion cells are Herpes Simplex Virus (HSV) vaccinia or adenovirus derived vectors. Viral vectors for use in gene therapy are discussed by Vile (1997) Nature Biotechnology 15: 840-841. A non-viral gene therapy approach is discussed by Sebestyen et al (1998) Nature Biotechnology 16: 80-85. The use of a variety of gene therapy delivery systems (including HSV VP22) is discussed by Fernandez & Baylay (1998) Nature Biotechnology 16: 418-420 and references therein.

Where the antisense down-regulating DNA or RNA is provided in dorsal root ganglia cells it potentially inhibits the pain response by actually decreasing the number of SPASIC channels on the surface of sensory cells. Where the antisense down-regulating DNA or RNA is provided in the central nervous system, it alters neurotransmitter release by actually decreasing the number of SPASIC channels on the surface of neurons.

Thus a nucleotide sequence which is complementary to any of the coding-nucleic acids discussed in relation to earlier aspects of the invention forms one part of the present invention.

The invention further provides a method of influencing the electrophysiological and pharmacological properties of a cell, said method comprising the step of causing or allowing expression of a heterologous nucleic acid sequence as discussed above within that cells, which may optionally be within an organism.

The present invention further provides the use of the nucleotide sequence of Seq ID No 1, or its complement, or a variant of either for down-regulation of gene expression, particularly down-regulation of expression of an ion channel-encoding gene, more preferably a cation channel, most preferably SPASIC.

In a further aspect of the present invention there is provided nucleic acid (e.g. antisense DNA) of the present invention for use in gene therapy, or for use in the preparation of medicaments for use in gene therapy.

In a further aspect of the present invention there is disclosed an organism, preferably a non-human mammal, comprising cells in which the activity of SPASIC or a variant thereof have been altered, preferably impaired, by use of the methods and materials discussed above. Particularly preferred is a rodent e.g. murine organism. Methods of producing 'knock out' mammals in which specific gene activities have been impaired are now well known to those skilled in the art - see e.g. Boerrigter et al (1995) Nature 377: 657-659, or Gossen and Vijk (1993) Trends Genet 9: 27-31.

In a further aspect of the present invention there is provided use of a protein, a transformed or transfected cell, or a transgenic organism as described above, for identifying a substance as having ion-channel modulating activity.

Such substances may, for instance, act as agonist, partial agonist or antagonist.

Thus the protein or cell may be used in a method comprising exposing the protein (e.g which is associated

with a membrane, for instance of a liposome) or cell surface to a solution of the substance such as to allow interaction between the substance and the SPASIC (or variant SPASIC) protein in the membrane and then measuring the electrophysiological response of the cell or membrane to this interaction. This measurement may optionally be compared with a reference figure.

Typically the response may be measured by use of a microelectrode technique accompanied by such measurement strategies as voltage clamping of the cell whereby activation of ion channels may be identified by inward or outward current flow as detected using the microelectrodes. ^{22}Na, ^{86}Rb, ^{45}Ca radiolabeled cations or ^{14}C or ^{3}H guanidine may be used to assess such ion flux; a sodium, calcium or potassium ion sensitive dye (such as Fura-2, or indo) may be used to monitor ion passage through the receptor ion channel, or a potential sensitive dye may be used to monitor potential changes, e.g. such as in depolarization.

Agonists and partial agonists may be identified by their relative efficacy as compared to extracellular acid pH or other known agonists in activating the receptor or, in the case of partial agonists and antagonists, by their ability to block the activation caused by a given acidity, for example pH 6, or other known agonists.

Such substances will have potential as analgesics or other neuromodulatory agents, and as such form a further aspect of the present invention, optionally in the form medicamanents (e.g. compositions comprising a pharmaceutically acceptable carrier or filler).

Purified SPASIC protein, or a variant thereof, e.g.

produced recombinantly by expression from encoding nucleic acid therefor, may be used to raise antibodies employing techniques which are standard in the art.

Antibodies and polypeptides comprising antigen-binding fragments of antibodies may be used (*inter alia*) as antagonists or inhibitors, or for use in identifying homologues.

Methods of producing antibodies include immunising a mammal with the protein or a fragment thereof. Antibodies may be obtained from immunised animals using any of a variety of techniques known in the art, and might be screened, preferably using binding of antibody to antigen of interest.

For instance, Western blotting techniques or immunoprecipitation may be used (Armitage et al, 1992, Nature 357: 80-82). Antibodies may be polyclonal or monoclonal.

Antibodies may be modified in a number of ways. Indeed the term "antibody" should be construed as covering any specific binding substance having a binding domain with the required specificity. Thus, this term covers antibody fragments, derivatives, functional equivalents and homologues of antibodies, including any polypeptide comprising an immunoglobulin binding domain, whether natural or synthetic. Chimaeric molecules comprising an immunoglobulin binding domain, or equivalent, fused to another polypeptide are therefore included. Cloning and expression of Chimaeric antibodies are described in EP-A-0120694 and EP-A-0125023. It has been shown that fragments of a whole antibody can perform the function of binding antigens. Examples of binding fragments are (i)

the Fab fragment consisting of VL, VH, CL and CH1 domains; (ii) the Fd fragment consisting of the VH and CH1 domains; (iii) the Fv fragment consisting of the Vl and VH domains of a single antibody; (iv) the dAb fragment (Ward, E.S. et al., Nature 341, 544-546 (1989) which consists of a VH domain; (v) isolated CDR regions; (vi) F(ab')2 fragments, a bivalent fragment comprising two linked Fab fragments (vii) single chain Fv molecules (scFv), wherein a VH domain and a VL domain are linked by a peptide linker which allows the two domains to associate to form an antigen binding site (Bird et al, Science, 242, 423-426, 1988; Huston et al, PNAS USA, 85, 5879-5883, 1988); (viii) bispecific single chain Fv dimers (PCT/US92/09965) and (ix) "diabodies", multivalent or multispecific fragments constructed by gene fusion (WO94/13804; P Holliger et al Proc. Natl. Acad. Sci. USA 90 6444-6448, 1993).

The present invention will now be described by way of illustration only by reference to the following non-limiting Figures, Sequence Listing and Examples. Further embodiments of the invention falling into the scope of the claims provided herewith will occur to those of ordinary skill in the art in the light of these.

Figures

Fig 1: Aligned amino acid sequences of SPASIC (protein of present invention), DRASIC (see Waldmann and Lazdunski 1998, Current Biology 8: 418-424); ASIC-alpha (also referred to as 'ASIC' - see also Waldmann and Lazdunski *supra*); ASIC-beta (GB 9718365.1 - unpublished at the filing date of the present application). Trans-membrane helices (TM1/TM2) are marked.

Fig 2: Shows a time-course the inward current (in pA) evoked by application of low pH (about 5) to a COS cell expressing SPASIC. The characteristic sustained inward current is clearly visible.

Sequence listings

The listing provided herewith gives the DNA and amino acid sequences of the following examples of the invention. Numbering of primers is with respect to Seq ID Nos 1 and 2 as appropriate.

SEQ ID No 1: cDNA corresponding to SPASIC cDNA as derived from Rattus norvegicus dorsal root ganglia cells.

SEQ ID No 2: Amino acid sequence of SPASIC protein from Rattus norvegicus dorsal root ganglia cells.

SEQ ID No 3: Amino acid sequence of ASIC protein of the prior art.

SEQ ID No 4: Primer for use with that of SEQ ID No 5 PCR screening (253-277)

SEQ ID No 5: Primer for use with that of SEQ ID No 4 in PCR screening (reverse 1955-1980)

SEQ ID No 6: Primer for use with that of SEQ ID No 7 in PCR screening (419-438)

SEQ ID No 7: Primer for use with that of SEQ ID No 6 in PCR screening (reverse 984-1008)

SEQ ID No 8: Primer for use with that of SEQ ID No 9 in

degenerate PCR screening (corresponds to amino acid sequence RYG/AKEI/LSM - numbers 379-386).

SEQ ID No 9: Primer for use with that of SEQ ID No 8 in PCR screening (corresponds, in reverse, to amino acid sequence GLFIGASI/L in the TM2 region of Figure 1 - numbers 438-445).

Examples

Example 1: Isolation of SPASIC

The rat ASIC-beta clone (Patent application GB 9718365.1) was used to probe a cDNA library. 10^6 clones from a size fractionated (2-4kb) DRG cDNA library were amplified on HyBond N+ filters (Amersham) prior to hybridisation (Woo et al. PNAS (1978) 75, 3688) 32-P dATP random-primed ASIC-beta EcoRI probe (position 1-2087) was used to probe the library. The filters were hybridised at low stringency in 6 x SSC, 0.5% SDS, 5 x Denhardt's solution, with 200 micrograms/ml boiled salmon sperm DNA at 53°C. The filters were washed briefly in 4 x SSC at room temperature, then twice in 2 x SSC with 0.5% SDS at 55°C for 20 minutes. The filters were autoradiographed for 3 days on Kodak X-Omat films.

The ASIC-beta EcoRI probe (position 1-2087) was also used for high stringency screening where the filters were given a final wash in 0.1 x SSC, 0.5% SDS at 68°C (Chen et al. 1995 Nature 377, 428-432). Plaques that hybridised at low stringency but not at high stringency were selected for secondary screening, followed by cross-hybridisation. Full length SPASIC clones were isolated in this way.

Example 2: Preparation of cDNA from *E. coli*

Bluescript plasmid DNA encoding for the protein of the invention was purified from the E. coli DNA by solvent extraction, Magic minipreps or Caesium chloride centrifugation, and digested with endonucleases EcoRI and XhoI targeted at the 3'-polylinker downstream of the cDNA and the site of the vector bacteriophage polymerase.

Example 3: Homology Cloning of other mammalian SPASIC using sequence derived from the rat cDNA clone.

Dorsal root ganglia or central nervous system tissue are isolated from available human or other mammalian source tissue in accordance with methods well known to those skilled in the art. RNA is extracted from the isolated tissue by extraction in guanidine or other chaotropic agents, followed by solvent extraction using phenol, phenol/chloroform and precipitation using isopropanol and ethanol (see Chomczynski & Sacchi, 1987, Anal Biochem 162: 156-159).

The isolated RNA is Northern blotted with probes derived from the SEQ ID No 1 to identify transcript size of candidate human clones. Messenger RNA from the RNA pool is extracted using oligo-dT cellulose or poly-U sepharose chromatography and cDNA is constructed from this RNA using reverse transcriptase (SuperScript) and DNA ligase. Double-stranded DNA is constructed and a directional cDNA library generated using lambda zap, lambda express, pcDNA, or other suitable vectors.

The 3' untranslated region of the SPASIC clone is sub-cloned into a plasmid vector (Bluescript or similar) followed by cutting out the insert and isolating it on

agarose gels. cRNA clones are labelled by *in vitro* transcription with SP6, T3 or T7 polymerases and ^{32}P or DIG labelled nucleotides. Alternatively the insert is radiolabelled by random prime or nick translation with ^{32}P or DIG-labelled nucleotides.

The cDNA library is screened by moderate stringency hybridisation to 50-60°C 5 x SSC, using radiolabelled or other labelled DNA or cRNA probes derived from the 3'-UTR of the DNA/RNA sequence. Alternatively, other regions of the protein may be used. Resulting clones are plaque purified and their insert sized examined. Cross hybridisation of the clones follows with isolation of individual distinct clones. Clones that contain inserts that correspond approximately to the size of human mRNAs determined by Northern blotting are isolated. cRNA is generated from the selected clones and injected into Xenopus oocytes or COS (up to 50nls, 1mg/ml) and using twin electrode voltage clamp studies, the expression of functional proton-gated channels investigated.

Functionally active channel clones have their insert DNA sequenced and this DNA is recloned into a selectable shuttle vector (e.g. pcDNA neo- Invitrogen) to generate transiently or permanently transfected cell lines (COS cells, CHO cells, 293 cells etc.) expressing functional human ASIC protein clones. These cell lines may then be used with either ^{22}Na, ^{86}Rb, ^{45}Ca ion flux measurement, electrophysiology or Na or Ca-sensitive dye techniques to provide a high-throughput screen for channel agonist or antagonist candidate compounds.

Example 4: PCR cloning of other mammalian SPASIC using sequence derived from the rat cDNA clone.

Dorsal root ganglia and spinal cord are are isolated from available human or other mammalian tissue material. RNA is extracted from the isolated tissue by extraction in guanidine or other chaotropic agents, followed by solvent extraction using phenol, phenol/chloroform and precipitation using isopropanol and ethanol. Random primers and reverse transcriptase are used to generate cDNA from the extracted human RNA using either total or poly A+ RNA.

Degenerate PCR primers derived from conserved regions of SEQ ID No-1 are used to amplify the cDNA using the polymerase chain reaction; e.g. using degenerate primer sequences SEQ ID No 4 and 5, 6 and 7 and 8 and 9. The products of the PCR reaction are separated on agarose gels and examined with products of the approximate predicted size being extracted and cloned into a pGemT vector. The clones are sequenced and the sequences examined for similarity with that of SEQ ID No 1. Candidate PCR fractions are used to screen a human cDNA DRG library as described in Example 2.

Example 5: *In vitro* expression of proton gated ASIC channels.

Plasmids encoding SPASIC cDNA are cut with restriction enzymes XhoI and EcoRI. The SPASIC insert, which comprises the protein encoding regions, is isolated from low melting agarose gel, and subcloned into pTracer-CMV and pgw1 vectors respectively between EcoRI and XhoI restriction sites. The orientation of these constructs is checked by sequencing.

Shuttle vectors eg. pTracer-CMV or pgw1 containing SPASIC were purified from maxipreps. These vectors were used to

express proton-gated channels by transfecting permanent cell line COS cells. Cultured COS cells from a 100 mm petri dish (80-90% confluent) were trypsinised and resuspended in 350 microlitres of ice cold HEBS buffer. 20-30 micrograms of plasmids of interest were dissolved with 150 microlitres of HEBS buffer, then mixed with the COS cell suspension in an electroporation cuvette and kept on ice to cool for 5 minutes. Meanwhile, the electroporator (Invitrogen) was set up at 250 microFarad, and charged for 3 minutes at 330V, 25mA, and 25W. The cuvette was flicked to resuspend cells and electroporation effected.

After transfection by electroporation, COS cells were seeded in low density in-30mm petri dish and cultured with 2ml MEM/10% FCS at 37°C for 2-3 days. The transfected cells were washed with buffer (in mM NaCl 146, KCl 5, $CaCl_2$ 2, MgCl2 1, Glucose 10, HEPES 10 at various pHs) and using the whole cell configuration of the patch-clamp technique, currents evoked by perfusing with low pH buffer (pH 5) were measured at a holding potential of -60mV, with a 20 second perfusion duration of pH 5 buffer (see Figure 2). Compounds to be assessed as agonists, partial agonists or antagonists of the ASIC channels were bath applied and inward current used as measurement of the activation or block of channels encoded by the transfected vectors.

Example 6: *Screening for ion channel modulating agents*

Permanently or transiently transfected COS cell lines expressing SPASIC are loaded with C-14 guanidine (10 microcuries per ml) in multiwell plates for 1 hour at 37°C in DHEM growth medium containing 10% calf serum, washed in Hepes buffered saline (pH 7.4) 4 times, and

rates of radioactivity released measured in the presence and absence of a low pH stimulus (pH 5.5 Hepes buffered saline), with or without the addition of compounds that may show agonist, partial agonist or antagonist activity (Wood et al, 1989 J Neurochem 53: 1203-1211).

Alternatively, permanently or transiently transfected COS cell lines in multiwell plates expressing SPASIC are loaded with potential-sensitive carbocynanine dyes and the fluorescence emission spectral response is observed following application of a low pH stimulus (pH 5.5 Hepes buffered saline). The response in the presence and absence of the putative activating compound is compared (see Am J Physiol 266, C37 1994).